

SEQUENCE LISTING

5 GENERAL INFORMATION:

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(120) TITLE OF THE INVENTION:

(130) FILE REFERENCE:

15 (A) Medium type: Diskette
(B) Computer: IBM compatible
(C) Operating system: Windows 98
(D) Software: Word 6.0

20 (150) Earlier patent application:

(A) Application number: NO 19992786
(B) Filing date: 08-JUN-1999

25 (160) NUMBER OF SEQUENCE ID NOS: 2

(210)

INFORMATION FOR SEQ ID NO: 1

(i) Sequence characteristics:

5 (A) Length: .. amino acid residues
(B) Type: amino acid
(D) Topology: single

(xi) Sequence description: SEQ ID NO: 1

10 Glu Phe Lys Phe Leu Pro Pro Pro Gly Tyr
1 5 10
Ala Pro Cys His Glu Ala Val Leu Pro Arg
15 15 20
Glu Arg Leu Arg Leu Glu Pro Ile Lys Glu
25 25 30
Tyr Arg Arg Glu Gly Pro Arg Gly Pro His
35 35 40
Leu Val Gly Pro Ser Arg Cys Leu Ser His
45 45 50
20 Thr Asp Phe Val Pro Cys Pro Val Asp Thr
55 55 60
Val Gln Ile Val Leu Pro Pro His Leu Glu
65 65 70
Arg Ile Arg Glu Lys Leu Ala Glu Asn Ile
75 75 80
25 His Glu Leu Trp Ala Leu Thr Arg Ile Glu
85 85 90
Gln Gly Trp Thr Tyr Gly Pro Val Arg Asp
95 95 100
30 Asp Asn Lys Arg Leu His Pro Cys Leu Val
105 105 110
Asn Phe His Ser Leu Pro Glu Pro Glu Arg
115 115 120
Asn Tyr Asn Leu Gln Met Ser Gly Glu Thr
35 125 130
Leu Lys Thr Leu Leu Ala Leu Gly Cys His
135 135 140
Val Gly Met Ala Asp Glu Lys Ala Glu Asp
145 145 150
40 Asn Leu Lys Lys Thr Lys Leu Pro Lys Thr
155 155 160
Tyr Met Met Ser Asn Gly Tyr Lys Pro Ala
165 165 170
45 Pro Leu Asp Leu Ser His Val Arg Leu Thr
175 175 180
Pro Ala Gln Thr Thr Leu Val Asp Arg Leu
185 185 190
Ala Glu Asn Gly His Asn Val Trp Ala Arg
195 195 200
50 Asp Arg Val Ala Gln Gly Trp Ser Tyr Ser

	205	210
	Ala Val Gln Asp Ile Pro Ala Arg Arg Asn	
	215	220
	Pro Arg Leu Val Pro Tyr Arg Leu Leu Asp	
5	225	230
	Glu Ala Thr Lys Arg Ser Asn Arg Asp Ser	
	235	240
	Leu Cys Gln Ala Val Arg Thr Leu Leu Gly	
	245	250
10	Tyr Gly Tyr Asn Ile Glu Pro Pro Asp Gln	
	255	260
	Glu Pro Ser Gln Val Glu Asn Gln Ser Arg	
	265	270
	Trp Asp Arg Val Arg Ile Phe Arg Ala Glu	
15	275	280
	Lys Ser Tyr Thr Val Gln Ser Gly Arg Trp	
	285	290
	Tyr Phe Glu Phe Glu Ala Val Thr Thr Gly	
	295	300
20	Glu Met Arg Val Gly Trp Ala Arg Pro Glu	
	205	310
	Leu Arg Pro Asp Val Glu Leu Gly Ala Asp	
	315	320
	Glu Leu Ala Tyr Val Phe Asn Gly His Arg	
25	325	330
	Gly Gln Arg Trp His Leu Gly Ser Glu Pro	
	335	340
	Phe Gly Arg Pro Trp Gln Ser Gly Asp Val	
	345	350
30	Val Gly Cys Met Ile Asp Leu Thr Glu Asn	
	355	360
	Thr Ile Ile Phe Thr Leu Asn Gly Glu Val	
	365	370
	Leu Met Ser Asp	
35		374

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INFORMATION FOR SEQ ID NO: 2

(i) Sequence characteristics:

5 (A) Length: .. amino acid residues
(B) Type: amino acid
(D) Topology: single

(xi) Sequence description: SEQ ID NO: 2

10 Arg Gly Arg Ser Leu Thr Lys Ala Gln Arg
1 5 10
Asp Val Ile Glu Asp Cys Leu Met Ala Leu
15 20
Cys Arg Tyr Ile Arg Pro Ser Met Leu Gln
25 30
His Leu Leu Arg Arg Leu Val Phe Asp Val
35 40
Pro Ile Leu Asn Glu Phe Ala Lys Met Pro
45 50
20 Leu Lys Leu Leu Thr Asn His Tyr Glu Arg
55 60
Cys Trp Lys Tyr Tyr Cys Leu Pro Thr Gly
65 70
Trp Ala Asn Phe Gly Val Thr Ser Glu Glu
25 75 80
Glu Leu His Leu Thr Arg Lys Leu Phe Trp
85 90
Gly Ile Phe Asp Ser Leu Ala His Lys Lys
95 100
30 Tyr Asp Gln Glu Leu Tyr Arg Met Ala Met
105 110
Pro Cys Leu Cys Ala Ile Ala Gly Ala Leu
115 120
Pro Pro Asp Tyr Val Asp Ala Ser Tyr Ser
35 125 130
Ser Lys Ala Glu Lys Lys Ala Thr Val Asp
135 140
Ala Glu Gly Asn Phe Asp Pro Arg Pro Val
145 150
40 Glu Thr Leu Asn Val Ile Ile Pro Glu Lys
155 160
Leu Asp Ser Phe Ile Asn Lys Phe Ala Glu
165 170
Tyr Thr His Glu Lys Trp Ala Phe Asp Lys
45 175 180
Ile Gln Asn Asn Trp Ser Tyr Gly Glu Asn
185 190
Val Asp Glu Glu Leu Lys Thr His Pro Met
195 200
50 Leu Arg Pro Tyr Lys Thr Phe Ser Glu Lys

	205	210
	Asp Lys Glu Ile Tyr Arg Trp Pro Ile Lys	
	215	220
	Glu Ser Leu Lys Ala Met Ile Ala Trp Glu	
5	225	230
	Trp Thr Ile Glu Lys Ala Arg Glu Gly Glu	
	235	240
	Glu Glu Arg Thr Glu Lys Lys Lys Thr Arg	
	245	250
10	Lys Ile Ser Gln Thr Ala Gln Thr Tyr Asp	
	255	260
	Pro Arg Glu Gly Tyr Asn Pro Gln Pro Pro	
	265	270
	Asp Leu Ser Gly Val Thr Leu Ser Arg Glu	
15	275	280
	Leu Gln Ala Met Ala Glu Gln Leu Ala Glu	
	285	290
	Asn Tyr His Asn Thr Trp Gly Arg Lys Lys	
	295	300
20	Lys Gln Glu Leu Glu Ala Lys Gly Gly	
	305	310
	Thr His Pro Leu Leu Val Pro Tyr Asp Thr	
	315	320
	Leu Thr Ala Lys Glu Lys Ala Arg Asp Arg	
25	325	330
	Glu Lys Ala Gln Glu Leu Leu Lys Phe Leu	
	335	340
	Gln Met Asn Gly Tyr Ala Val Thr	
	345	348